

Result No.	Score	Query	Match	Length	DB ID	Description	
1	3369	100.0	652	9	US-09-837-992.1	Sequence 1, Appli	
2	3369	100.0	652	10	US-09-837-991A-2	Sequence 2, Appli	
3	2744.5	81.5	651	9	US-09-837-992.3	Sequence 3, Appli	
4	2744.5	81.5	651	10	US-09-837-991A-6	Sequence 4, Appli	
5	2744.5	81.5	651	14	US-10-090-451-6	Sequence 5, Appli	
6	1177	34.9	256	15	US-10-104-041-2795	Sequence 6, Appli	
7	701.5	20.8	672	10	US-09-989-991A-4	Sequence 7, Appli	
8	691.5	20.6	655	10	US-09-961-061-1	Sequence 8, Appli	
9	691.5	20.6	655	15	US-10-061-061-13	Sequence 9, Appli	
10	691.5	20.5	655	14	US-10-120-687-61	Sequence 10, Appli	
11	691.5	20.5	655	15	US-10-061-061-2	Sequence 11, Appli	
12	691.5	20.5	655	9	US-09-866-866-10	Sequence 12, Appli	
13	689.5	20.5	655	14	US-10-090-445-5	Sequence 13, Appli	
14	689.5	20.5	673	10	US-09-989-981A-8	Sequence 14, Appli	
15	688.5	20.4	673	14	US-10-090-455-7	Sequence 15, Appli	
16	688.5	20.3	655	9	US-09-866-866A-27	Sequence 16, Appli	
17	683.5	20.1	657	9	US-09-866-866A-14	Sequence 17, Appli	
18	677	19	628	18.6	1095	Sequence 18, Appli	
			619	18.4	725	Sequence 19, Appli	
			602.5	17.9	1049	Sequence 20, Appli	
			22	592.5	17.6	674	Sequence 21, Appli
			23	592.5	17.6	674	Sequence 22, Appli
			24	586	17.4	663	Sequence 23, Appli
			25	584.5	17.3	1084	Sequence 24, Appli
			26	584.5	17.3	1101	Sequence 25, Appli
			27	580	17.2	638	Sequence 26, Appli
			28	579.5	17.2	658	Sequence 27, Appli
			29	576.5	17.1	646	Sequence 28, Appli
			30	576.5	17.1	646	Sequence 29, Appli
			31	574.5	17.1	599	Sequence 30, Appli
			32	573.5	17.0	608	Sequence 31, Appli
			33	573.5	17.0	695	Sequence 32, Appli
			34	571.5	17.0	623	Sequence 33, Appli
			35	570	16.9	559	Sequence 34, Appli
			36	569.5	16.9	627	Sequence 35, Appli
			37	569	16.9	604	Sequence 36, Appli
			38	562.5	16.7	646	Sequence 37, Appli
			39	561.5	16.7	819	Sequence 38, Appli
			40	558.5	16.6	646	Sequence 39, Appli
			41	555.5	16.5	646	Sequence 40, Appli
			42	554.5	16.5	646	Sequence 41, Appli
			43	554	16.4	610	Sequence 42, Appli
			44	537.5	16.0	656	Sequence 43, Appli
			45	537.5	16.0	673	Sequence 44, Appli





Query Match 81.5%; Score 2744.5; DB 14; Length 651;  
 Best Local Similarity 80.2%; Pred. No. 1.8e-258; Indels 1; Gaps 1;  
 Matches 523; Conservative 64; Mismatches 6; Insertions 1;

Qy 1 MGEELPFSPGARGPRHNGSLSLLEQGSVTGPARHSIGLUVLHVSYSVSNRGPWNNTKS 60  
 Db 1 MGDLSSLTPGGSMGLQVNRSQSSEGAATAPBP-HSIGLHASYSVSHTRPWWDLTS 59

Qy 61 CQQRDQIQRKDVSILYTESQIMCLGSQSCKTLLDLSIGRURRITLLEGAVFVNGC 120  
 Db 60 CQQWTRQIQLKDVSILYTESQIMCLGSQSCKTLLDMSGRGAGFELGEVYNGRA 119

Qy 121 LRRDQFQDCFSXYLQSDVFLSSLTRETRIYTAALCROSSADEFYKKEATMTELSLSH 180  
 Db 122 LRRDQFQDCFSXYLQSDVFLSSLTRETRIYTAALCROSSADEFYKKEATMTELSLSH 179

Qy 181 VADOMIGSTXNGFQGSSGERRVSTAQQIQLQDPKWMIDPPTTGLDCMTANQIVLLAELA 240  
 Db 180 VADRLIGNSYGGTIGERRVSTAQQIQLQDPKWMIDPPTTGLDCMTANQIVLLAELA 239

Qy 241 RDRDIVTITIOPRSELEQHDKIAITYGELBVECGTPPEMIGPENNGCPCDEHSNPF 300  
 Db 240 RRNRTIVLTHQPRSELIQFDKTAILSFBLIGTPPEMIDFNDCCYPCBHSNPF 299

RESULT 7  
 US-09-989-981A-4  
 Sequence 4; Application US/09989981A  
 Publication No. US20030049730A1  
 GENERAL INFORMATION:  
 APPLICANT: Hobbs, Helen H.  
 APPLICANT: Shar, Bei  
 APPLICANT: Barnes, Robert  
 APPLICANT: Tian, Hui  
 APPLICANT: Tularik Inc.  
 APPLICANT: Board of Regents, The University of Texas System  
 TITLE OF INVENTION: ABCG8 and ABCG8: Compositions and Methods of Use  
 FILE REFERENCE: 018781-007200US  
 CURRENT APPLICATION NUMBER: US/09/989, 981A  
 CURRENT FILING DATE: 2002-07-23  
 PRIOR APPLICATION NUMBER: US 60/252, 235  
 PRIOR FILING DATE: 2000-11-20  
 PRIOR APPLICATION NUMBER: US 60/253, 645  
 PRIOR FILING DATE: 2000-11-28  
 NUMBER OF SEQ ID NOS: 13  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO 4  
 LENGTH: 672  
 TYPE: PRT  
 ORGANISM: Mus musculus  
 FEATURE:  
 OTHER INFORMATION: mouse ABCG8 (mABCGB8)  
 US-09-989-981A-4

Query Match 80.8%; Score 701.5; DB 10; Length 672;  
 Best Local Similarity 29.1%; Pred. No. 5.5e-39; Gaps 19;  
 Matches 194; Conservative 131; Mismatches 245; Indels 97;

Qy 420 VGLLYQVFGATPTGMLNAYNLFPMLRAYSQESDGLQKQWMLLAZLHVLPSVVA 479  
 Db 420 VGLLYQVFGATPTGMLNAYNLFPMLRAYSQESDGLQKQWMLLAZLHVLPSVVA 479

Qy 481 VIFSSVCYWTLGLYPEVARFQYFSALLAALPHIGFLTLVLLGIVONPNIVNSIVALLSI 540  
 Db 480 MIFSSVCYWTLGLHPEVARFQYFSALLAALPHIGFLTLVLLGIVONPNIVNSIVALLSI 539

Qy 541 SGLIGSGFIRNQIENQMPIKILGYTFQKCYCETLIVYNEFYGILNFTCGSNTSMLNHPM 600  
 Db 540 AGVLYESGFLNQIENQMPIKILGYTFQKCYCETLIVYNEFYGILNFTCGSNTSMLNHPM 599

Qy 601 CATTQGVFIRKTCPTATSRSTANFLIYGFIPALVIGVTFKVDYLISR 652  
 Db 600 CATTQGVFIRKTCPTATSRSTANFLIYGFIPALVIGVTFKVDYLISR 651

RESULT 6  
 US-10-104-047-2795  
 Publication No. US2003023639A1  
 GENERAL INFORMATION:  
 APPLICANT: HELIX RESEARCH INSTITUTE  
 TITLE OF INVENTION: No. US2003036392A1 full length cDNA  
 FILE REFERENCE: HL-A0105  
 CURRENT APPLICATION NUMBER: US10/104, 047  
 CURRENT FILING DATE: 2002-03-25  
 PRIOR APPLICATION NUMBER:  
 PRIOR FILING DATE:  
 NUMBER OF SEQ ID NOS: 4096  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO: 2795  
 LENGTH: 256  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-10-104-047-2795

Query Match 34.9%; Score 1177; DB 15; Length 256;  
 Best Local Similarity 85.5%; Pred. No. 4.6e-106; Mismatches 14; Indels 0; Gaps 0;

Qy 397 MGLFLIYLLRQVNNTLKGAVQDVRGLLYOLVGATPTGMLNAYNLFPMLRAYSQESDQ 456  
 Db 1 MGLFLIYLLRQVNNTLKGAVQDVRGLLYOLVGATPTGMLNAYNLFPMLRAYSQESDQ 60

Qy 457 GLYHKQMLLAIAYLHVLPFSVIAVTFESSVYCYWTLGLYPEVARFQYFSALLAALPHIGRF 516  
 Db 61 GLYHKQMLLAIAYLHVLPFSVIAVTFESSVYCYWTLGLHPEVARFQYFSALLAALPHIGRF 120

Qy 517 LTLVLIGIVQDNTNISTIVALLSISQLLGSGFIPNQMPIKILGYTFQKCYCETL 576  
 Db 121 LTLVLIGIVQDNTNISTIVALLSISQLLGSGFIPNQMPIKILGYTFQKCYCETL 180

Qy 577 VVNEFTGLNFNTGGSNTSMLNHPMCATQVFTKTCGATSRFTANFLIYGFIPALV 636  
 Db 181 VVNEFTGLNFNTGSSNTSMLNHPMCATQVFTKTCGATSRFTANFLIYGFIPALV 240

Qy 637 ILGIVIVFKVDYLISR 652  
 Db 241 ILGIVIVFKRDYLISR 256

Qy 640 ARDRDIVTIVTIEOPRSEI.FQHFKIALITYGELVFLVTFPTEENLGFNNNGCPCPESNPF 299  
 Matches 219; Conservative 23; Mismatches 14; Indels 0; Gaps 0;





Db	68	NGIMKPG-LNAILGPTCGKSSLLDVLAARKKDPG-LSGDVLINGAP-RPANFKCNSGYV 124	Db	68	NGIMKPG-LNAILGPTCGKSSLLDVLAARKKDPG-LSGDVLINGAP-RPANFKCNSGYV 124
Qy	134	IOSDVELSISLUTRETRYTAMALCRSSADF-YNKVEAYMTLSHADOMIGSYNNG 192	Qy	134	LGDFVFLSSLTRETRYTAMALCRSSADF-YNKVEAYMTLSHADOMIGSYNFG 192
Db	125	VODDVNGTLYTRENIQFSAAURLAATMNEBKNERINRVIQELLDKTDASKTGQPR 184	Db	125	VDDVNGTLYTRENIQFSAAURLAATMNEBKNERINRVIQELLDKTDASKTGQPR 184
Qy	193	GISSGERRVSTAAGLQDQPKWMMDEPTTGCDMTANQVLLAELAARRDRIVVTTIHQ 252	Qy	193	GISSGERRVSTAAGLQDQPKWMMDEPTTGCDMTANQVLLAELAARRDRIVVTTIHQ 252
Db	185	GVSGBEKRTSQGMELTDPSLFDLTDPSLFDLTDPSLFDLTDPSLFDLTDPSLFD 244	Db	185	GVSGBEKRTSQGMELTDPSLFDLTDPSLFDLTDPSLFDLTDPSLFDLTDPSLFD 244
Qy	253	PRSELQFHFDKIALITYGELYFCGTPPEMLGFPNNGYPCPEHSNPFDYMDLTSYDTQ- 311	Qy	253	PRSELQFHFDKIALITYGELYFCGTPPEMLGFPNNGYPCPEHSNPFDYMDLTSYDTQ- 311
Db	245	PRYSIFLFDSTLTLASGRMLMFHGPQAEALGYFESAGYHCEAYNNPAPDFFLDINGDSTA 304	Db	245	PRYSIFLFDSTLTLASGRMLMFHGPQAEALGYFESAGYHCEAYNNPAPDFFLDINGDSTA 304
Qy	312	-SRERELEYTYKRVQMLECAFESDITYHKI-----LENIEARYLKT 351	Qy	312	-SRERELEYTYKRVQMLECAFESDITYHKI-----LENIEARYLKT 351
Db	305	VALNRE-BDFKATEB1EBSQDKPLIEKLAETYVNSSFYKETKAELHQSGGGKKKITY 363	Db	305	VALNRE-BDFKATEB1EBSQDKPLIEKLAETYVNSSFYKETKAELHQSGGGKKKITY 363
Qy	352	LPMVPPFKTRKDPPGMFGKLGVLLRTRVNLMKNOAVTMRLYQNLIMGLFLFYLLRVQNN 411	Qy	352	LPMVPPFKTRKDPPGMFGKLGVLLRTRVNLMKNOAVTMRLYQNLIMGLFLFYLLRVQNN 411
Db	364	FKEISYTT---SFCHOIWTWSKRSFQNLLGPNQASIAQIIVTVVULGLVIGAIYFGKND 419	Db	364	FKEISYTT---SFCHOIWTWSKRSFQNLLGPNQASIAQIIVTVVULGLVIGAIYFGKND 419
Qy	412	TLKGAVODVRGLLQYOLVQATPTGMLNANVLFPMLRASDQESODGLYHNMQMLLAYVL- 470	Qy	412	TLKGAVODVRGLLQYOLVQATPTGMLNANVLFPMLRASDQESODGLYHNMQMLLAYVL- 470
Db	420	ST--GIORAGLFLITTNQCESS-VASELLEVVEKKFLFHYISGYRVSSYFLGKLLS 476	Db	420	ST--GIORAGLFLITTNQCESS-VASELLEVVEKKFLFHYISGYRVSSYFLGKLLS 476
Qy	471	HVLPFSVATIATVFSVSYWTGLYPEVAFRGYFSAAALLAAPHIGEFLTVLGLTIVONPNI 530	Qy	471	HVLPFSVATIATVFSVSYWTGLYPEVAFRGYFSAAALLAAPHIGEFLTVLGLTIVONPNI 530
Db	477	DLLPMPRMPSIIFTCTYFMLGKPKDAFFPMFTLM---MVAYSASRNLATAAGQSV 533	Db	477	DLLPMPRMPSIIFTCTYFMLGKPKDAFFPMFTLM---MVAYSASRNLATAAGQSV 533
Qy	531	VNSIVALLSIS--GLLIGSGFIRNIQEMPIPILKIGYPTQKYCCELIVNNEFYGLNFTC 588	Qy	531	VNSIVALLSIS--GLLIGSGFIRNIQEMPIPILKIGYPTQKYCCELIVNNEFYGLNFTC 588
Db	534	VSVATLMTICFVMMIFSGLVLNLTTIASWLSWQYFSIPTYGFTALQNEFLQNF-C 592	Db	534	VSVATLMTICFVMMIFSGLVLNLTTIASWLSWQYFSIPTYGFTALQNEFLQNF-C 592
Qy	589	GGNTSMMLAHNHPMCATITQGVQFIEK 612	Qy	589	GGNTSMMLAHNHPMCATITQGVQFIEK 612
Db	593	PGLNATGNNPNCNYATCTGEEYLVK 616	Db	593	PGLNATGNNPNCNYATCTGEEYLVK 616
RESULT 12					
US-10-405-806-2					
; Sequence 2, Application US/10405806					
; Publication No. US200302336241					
; GENERAL INFORMATION					
; APPLICANT: KONATANI, HIDEYA					
; APPLICANT: HARA, YOSHIAKU					
; APPLICANT: KOTANI, HIDEBITO					
; APPLICANT: NAKAGAWA, RINAKO					
; TITLE OF INVENTION: DRUG RESISTANT GENE AND USE THEREOF					
; CURRENT APPLICATION NUMBER: US/10/405_806					
; CURRENT FILING DATE: 2003-04-03					
; PRIORITY APPLICATION NUMBER: PCT/JP01/08112					
; PRIORITY FILING DATE: 2001-09-18					
; PRIORITY APPLICATION NUMBER: JP2000-303441					
; PRIORITY FILING DATE: 2000-10-03					
; NUMBER OF SEQ ID NOS: 17					
; SOFTWARE: Patentin version 3.2					
; SEQ ID NO 2					
; LENGTH: 655					
; TYPE: PRT					
; ORGANISM: Homo sapiens					
; US-10-405-806-2					
; Query Match Score 20.5%; DB 15; Length 655;					
; Best Local Similarity 29.0%; Pred. No. 5e-58;					
; Matches 181; Conservative 141; Mismatches 247; Indels 55; Gaps 16;					
; Query 25 LEQGSVTVGEARHS-----LGTVLHVSYSVSNRGPWNNIKSCQQKWDQILKDV 73					
; Db 12 VSQNTINGPFTATVSNDLKAFTEGAVLSSNTICRVLKSG---FLPCRKPVSEKILSNI 67					
; Query 74 SLYTESQQIMCILGSSGGCKTTLDAISGRRLRTGTLGEVFVNGCELLRRDOFQDCSYV 133					
; Query Match Score 20.5%; DB 9; Length 655;					
; Best Local Similarity 29.0%; Pred. No. 7.9e-58;					
; Matches 181; Conservative 141; Mismatches 247; Indels 55; Gaps 16;					
; Query 25 LEQGSVTVGEARHS-----LGTVLHVSYSVSNRGPWNNIKSCQQKWDQILKDV 73					
; Db 12 VSQNTINGPFTATVSNDLKAFTEGAVLSSNTICRVLKSG---FLPCRKPVSEKILSNI 67					



85 ILGSSGGKTLDAISGLRRTGTLLEGIVFVNGCELRDQFQDCFSYVQSDVFLSSLT 144  
 Db 103 IIGSSGGCRASILDVTRGKGGKIKSGQWINGQPSSPOLYRKVVAHYRQHNLLEPNLT 162  
 Qy 145 VRETLRYTAMIALCRS-SADFYNKVEAVENTELSLSHVAEOMIGSYNGFSTISSGERRRS 203  
 Db 163 VRETLAFIAQMLRPLPFSQARDKRYEDVIAELRURQCATRIVGMMYRVLSGGERRRS 222  
 Qy 204 TAAQLIQDPKYNMILDEPTGLDCMTANOTIVLLAELAARDRIVVTHIOPRSELFQHFDK 263  
 Db 223 IGVQLLWNPGLLDEPTGLDSFTAHNLVKTSLRAKGNRVLVLSLHQPSDFRLFL 282  
 Qy 264 IAILTYGELVFGTPEEMLGFNNNGCYPCPBHSNPFDYMDLTSYDTSQSREREIETYKV 323  
 Db 283 VLLMTSCTPIVYGAQMRVQYTAICYPCPYNSNPADFYVQLTSDRSSEQEALATRECA 342  
 Qy 324 QMLECAFKEFSDIYHKILLENARYL-----KTLPM----VPFXT 359  
 Db 343 QSLAALF-----LEKVRDQDDEFLWKAETKDLDEDTCYBESSVTPLDTNCLPSRT 390  
 Qy 360 KDPGGMFGKGLGVLLRRTVNLMRNKAOAVIRLBNQNLIMGFLIFYLRLRQNNTLKGAVQD 419  
 Db 391 K-MPGAVQQTFLIRRAISNDFDLTLLTHGAECIMSMTIGF-LYFSGHSIQLSFND 447  
 Qy 420 RVGLLXYLQVATPYTGMLNAVLPMLRAYSDOESDGLYRHKWONLAVLHLPFSVIA 479  
 Db 448 TAALLFMIGALIPENTVLDISKCYSERAMLYYELEDGLYTTGPFFAKLGELPEHCAY 507  
 Qy 480 TVIFSSYCYWTLGLYPEVAFP-----GYFSAAALLAAPHLIGEFLTLVIL 522  
 Db 508 IIIYGMPTWILANLRPGIQPFILLHFLWLVVFCCBIMALAALIPTMASFFSNAL- 566  
 Qy 523 GIVQNPVNIVNSTVALLSISGJLIGSGFIRNIOEMPIPLKILGYEDFOKCCELIVVNEP- 581  
 Db 567 -----YNSFYLAGGEMINISLWTVPAWISKOSFLRWFEGMVKIQS 609  
 Qy 582 ---YGL---NFTCGGSNTISML-----NHPMCATQGVQFLEKTPGATSRPTANFLILY 629  
 Db 610 RRTYKMPGNLTIAVSDKILSAMELDSYPAI-----YLIVI 648  
 Qy 630 GPTIPALVIL 638  
 Db 649 GLSGGPFWTL 657

Search completed: March 17, 2004, 19:53:48  
 Job time : 26.1148 secs